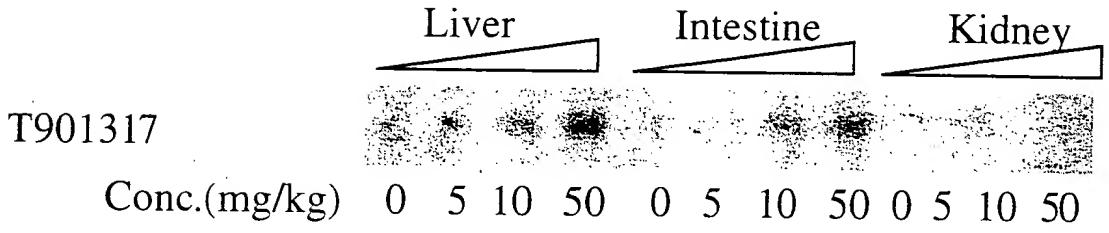
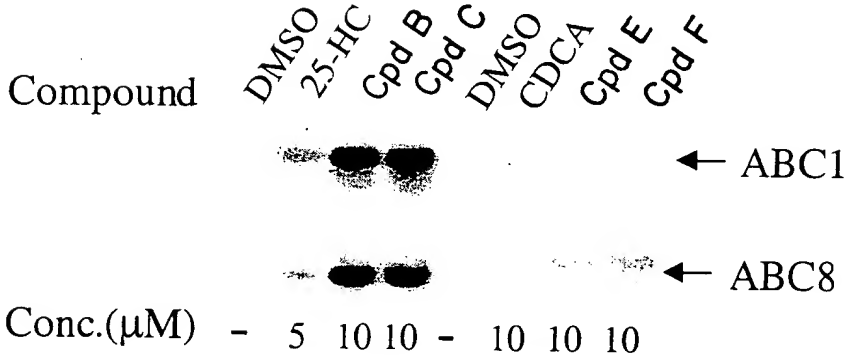


FIG. 1.



LXR agonist: Cpd B, C

FXR agonist: Cpd E, F

FIG. 2.

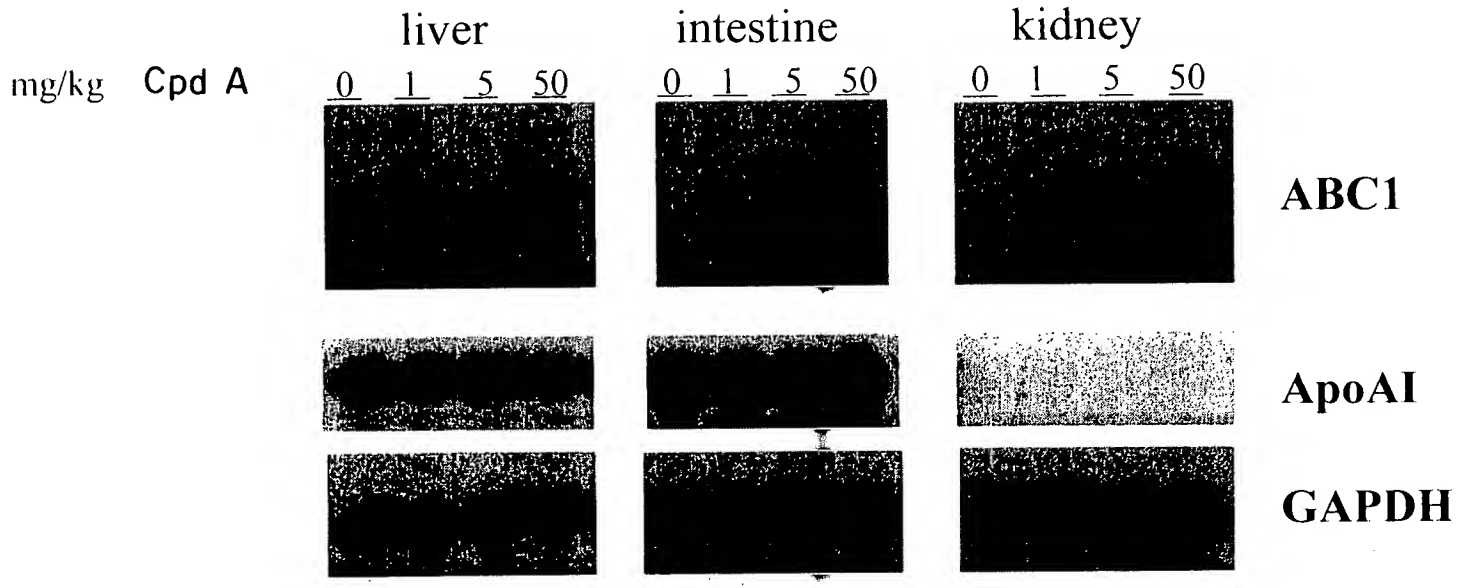

liver
intestine
kidney
mg/kg Cpd A
0 1 5 50
0 1 5 50
0 1 5 50
ABC1
ApoAI
GAPDH

FIG. 3.

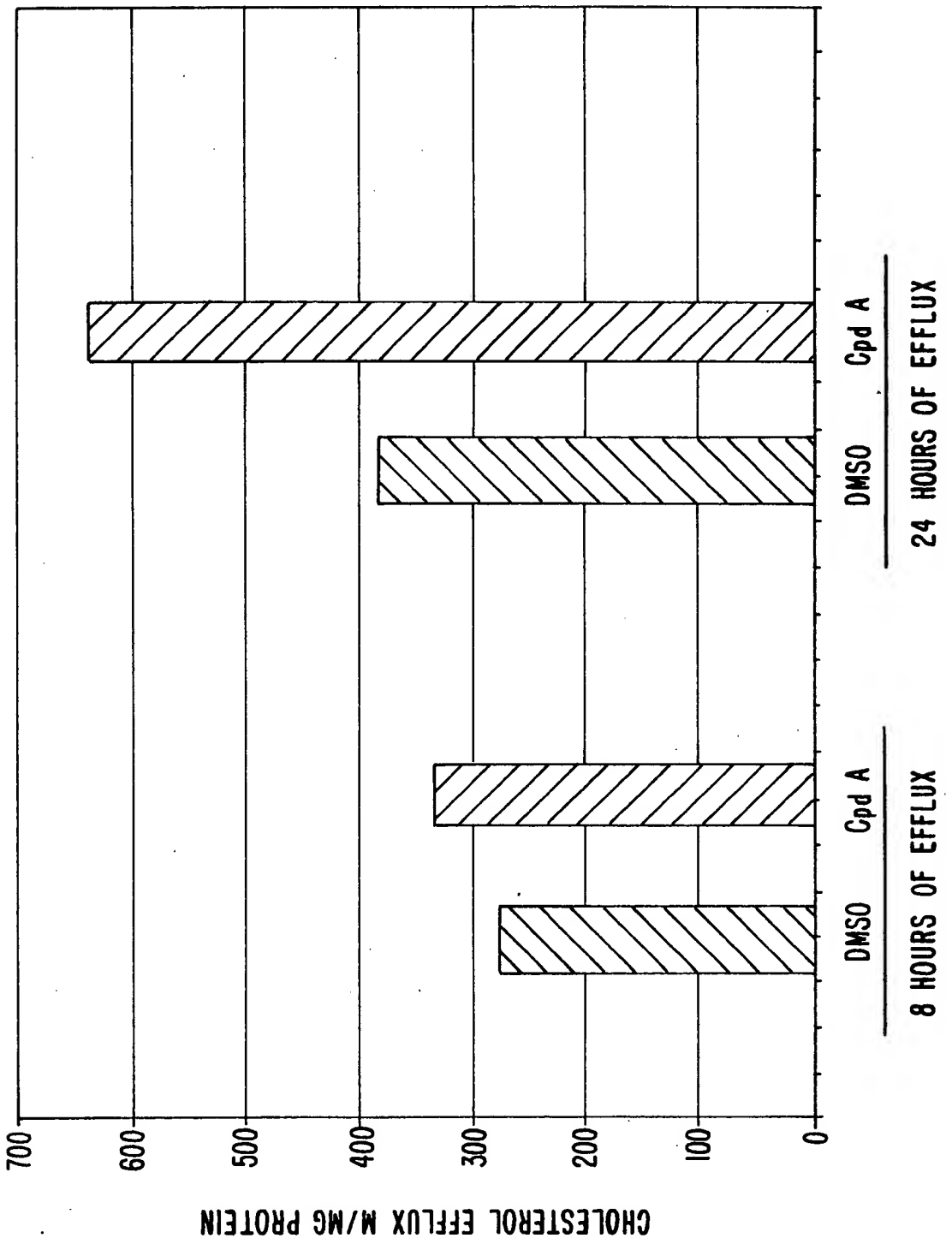

CHOLESTEROL EFFLUX M/MG PROTEIN
0
100
200
300
400
500
600
700
DMSO
Cpd A
8 HOURS OF EFFLUX
DMSO
Cpd A
24 HOURS OF EFFLUX

FIG. 4.

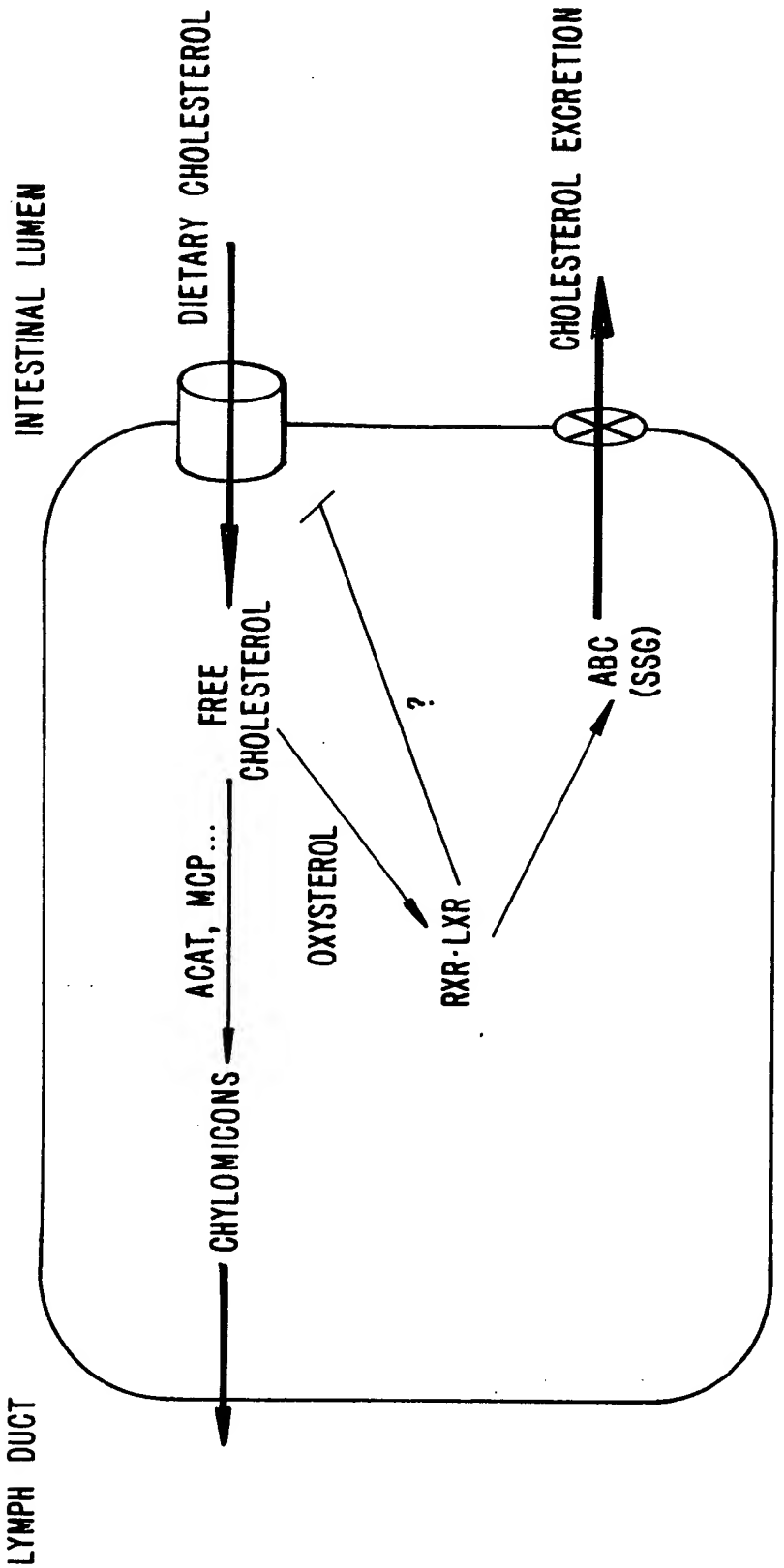
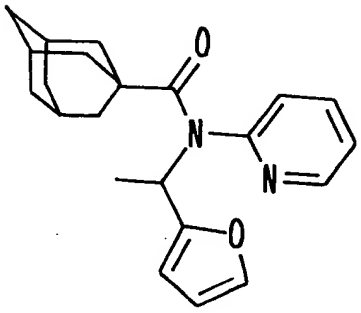
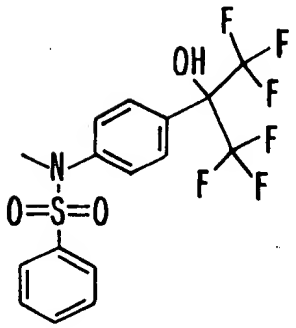

INTESTINAL LUMEN
DIETARY CHOLESTEROL
CHOLESTEROL EXCRETION
FREE CHOLESTEROL
ACAT, MCP...
CHYLOMICONS
OXYSTEROL
?
RXR·LXR
ABC (SSG)
LYMPH DUCT

FIG. 5.

COMPOUND C



COMPOUND B



COMPOUND A

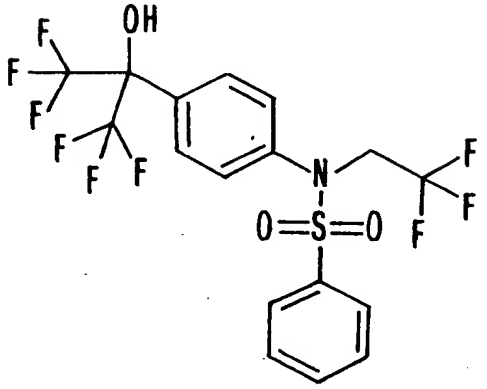


FIG. 6.

```
;ACAGGCCACTAGAAAATTCACTTGCATTTGCTTCCTGCTAGCCATGGGTGAGCTGCCCTTTCTGAGTCCAGAGGGAGCCAGAGGGCCTCACA   95
                                                M  G  E  L  P  F  L  S  P  E  G  A  R  G  P  H

ACAGAGGGTCTCTGAGCTCCCTGGAGCAAGGTTCGGTCACGGGCACAGAGGCTCGGCACAGCTTAGGTGTCCTGCATGTGTCCTACAGCGTC  190
N  R  G  S  L  S  S  L  E  Q  G  S  V  T  G  T  E  A  R  H  S  L  G  V  L  H  V  S  Y  S  V

AACCGTGTCGGGCCTTGGTGGAACATCAAATCATGCCAGCAGAAGTGGGACAGGCAAATCCTCAAAGATGTCTCCTTGTACATCGAGAGTGG  285
 N  R  V  G  P  W  W  N  I  K  S  C  Q  Q  K  W  D  R  Q  I  L  K  D  V  S  L  V  I  E  S  G

GATTATGTGCATCTTAGGCAGCTCAGGCTCAGGGAAGACCACGCTGCTGGACGCCATCTCCGGGAGGCTGCGGCGCACTGGGACCCTGGAAG  380
 I  M  C  I  L  G  S  S  G  S  G  K  T  T  L  L  D  A  I  S  G  R  L  R  R  T  G  T  L  E

AGGTGTTTGTGAATGGCTGCGAGCTGCGCAGGGACCAGTTCCAAGACTGCTTCTCCTACGTCCTGCAGAGCGACGTTTTTCTGAGCAGCCTC  475
E  V  F  V  N  G  C  E  L  R  R  D  Q  F  Q  D  C  F  S  Y  V  L  Q  S  D  V  F  L  S  S  L

GTGCGCGAGACGTTGCGATACACAGCGATGCTGGCCCTCTGCCGCAGCTCCGCGGACTTCTACAACAAGAAGGTAGAGGCAGTCATGACAGA  570
 V  R  E  T  L  R  Y  T  A  M  L  A  L  C  R  S  S  A  D  F  Y  N  K  K  V  E  A  V  M  T  E

GAGCCTGAGCCACGTGGCGGACCAAATGATTGGGAGCTATAATTTTGGGGGAATTTCCAGTGGCGAGCGGCGCCGAGTTTCCATCGCAGCCC  665
 S  L  S  H  V  A  D  Q  M  I  G  S  Y  N  F  G  G  I  S  S  G  E  R  R  R  V  S  I  A  A

TCCTTCAGGACCCCAAGGTCATGATGCTAGATGAGCCAACCACAGGACTGGACTGCATGACTGCAAATCAAATTGTCCTTCTCTTGGCTGAG  760
L  L  Q  D  P  K  V  M  M  L  D  E  P  T  T  G  L  D  C  M  T  A  N  Q  I  V  L  L  L  A  E

GCTCGCAGGGACCGAATTGTGATTGTCACCATCCACCAGCCTCGCTCTGAGCTCTTCCAACACTTCGACAAAATTGCCATCCTGACTTACGG  855
 A  R  R  D  R  I  V  I  V  T  I  H  Q  P  R  S  E  L  F  Q  H  F  D  K  I  A  I  L  T  Y  G

GTTGGTGTTCTGTGGCACCCCAGAGGAGATGCTTGGCTTCTTCAATAACTGTGGTTACCCCTGTCCTGAACATTCCAATCCCTTTGATTTTT  950
 L  V  F  C  G  T  P  E  E  M  L  G  F  F  N  N  C  G  Y  P  C  P  E  H  S  N  P  F  D  F

TGGACTTGACATCAGTGGACACCCAAAGCAGAGAGCGGGAAATAGAAACGTACAAGCGAGTACAGATGCTGGAATGTGCCTTCAAGGAATCT 1045
M  D  L  T  S  V  D  T  Q  S  R  E  R  E  I  E  T  Y  K  R  V  Q  M  L  E  C  A  F  K  E  S
```

FIG. 7A.

```
:ATCTATCACAAAATTCTGGAGAACATTGAAAGAGCACGATACCTGAAAACCTTACCCATGGTTCCTTTCAAAACAAAAGATCCTCCTGGGAT 1140
  I  Y  H  K  I  L  E  N  I  E  R  A  R  Y  L  K  T  L  P  M  V  P  F  K  T  K  D  P  P  G  M

'CGGCAAGCTTGGTGTCCTGCTGAGGCGAGTAACAAGAAACTTAATGAGGAATAAGCAGGCAGTGATTATGCGTCTCGTTCAGAATCTGATCA 1235
 ` G  K  L  G  V  L  L  R  R  V  T  R  N  L  M  R  N  K  Q  A  V  I  M  R  L  V  Q  N  L  I

;GCCTCTTCCTCATTTTCTACCTTCTCCGCGTCCAGAACAACACGCTAAAGGGCGCTGTGCAGGACCGCGTGGGGCTGCTCTATCAGCTTGTG 1330
 G  L  F  L  I  F  Y  L  L  R  V  Q  N  N  T  L  K  G  A  V  Q  D  R  V  G  L  L  Y  Q  L  V

'GCCACCCCATACACCGGCATGCTCAATGCTGTGAATCTGTTTCCCATGCTGAGAGCCGTCAGCGACCAGGAGAGTCAGGATGGCCTGTATCA 1425
  A  T  P  Y  T  G  M  L  N  A  V  N  L  F  P  M  L  R  A  V  S  D  Q  E  S  Q  D  G  L  Y  H

.GTGGCAGATGCTGCTCGCCTACGTGCTACACGTCCTCCCCTTCAGCGTCATCGCCACGGTCATTTTCAGCAGTGTGTGTTATTGGACTCTGG 1520
 : W  Q  M  L  L  A  Y  V  L  H  V  L  P  F  S  V  I  A  T  V  I  F  S  S  V  C  Y  W  T  L

'TGTATCCTGAAGTTGCCAGATTTGGATATTTCTCTGCTGCTCTTTTGGCCCCTCACTTAATTGGAGAATTTCTAACACTTGTGCTGCTTGGT 1615
 L  Y  P  E  V  A  R  F  G  Y  F  S  A  A  L  L  A  P  H  L  I  G  E  F  L  T  L  V  L  L  G

.GTCCAAAACCCTAATATTGTCAACAGTATAGTGGCTCTGCTCAGCATCTCTGGGCTGCTTATTGGATCTGGATTTATCAGAAACATACAAGA 1710
  V  Q  N  P  N  I  V  N  S  I  V  A  L  L  S  I  S  G  L  L  I  G  S  G  F  I  R  N  I  Q  E

GCCCATTCCTTTAAAAATCCTGGGTTATTTTACATTCCAAAAATACTGTTGTGAGATTCTCGTGGTCAATGAGTTTTACGGCCTGAACTTCA 1805
 : P  I  P  L  K  I  L  G  Y  F  T  F  Q  K  Y  C  C  E  I  L  V  V  N  E  F  Y  G  L  N  F

GTGGTGGATCCAACACCTCTATGCTAAATCACCCGATGTGCGCCATCACCCAAGGGGTCCAGTTCATCGAGAAAACCTGCCCAGGTGCTACA 1900
C  G  G  S  N  T  S  M  L  N  H  P  M  C  A  I  T  Q  G  V  Q  F  I  E  K  T  C  P  G  A  T

AGATTCACGGCAAACTTCCTCATCTTATATGGGTTTATCCCAGCTCTGGTCATCCTAGGAATAGTGATTTTTAAAGTCAGGGACTACCTGAT 1995
 R  F  T  A  N  F  L  I  L  Y  G  F  I  P  A  L  V  I  L  G  I  V  I  F  K  V  R  D  Y  L  I

CAGATAGTTAAGATGACAGGCAGGAAAGGGTTAATGGGCAGGCACGCCCACTGTGGAGCACAGAGAAGTACTGTCTTCAACCATCAGGATTC 2090
  R  X>
```

FIG. 7B.

```
CTGCGACCCTTGTGTCTGACCCTTGTGTCTATCCGGAGCCCCAAGGGCAACGAGAACTCACAGCCCTCTGCTATTCCAGCTTGTGGGGCAAT 2185

GTGCTTGGACATTGTGACTGAACTGGTCCAATAATGTAAATAATAATAATTCATAAACCTACAGGACATT                      2258
```

FIG. 7C.

```
AGGTGGAGCAGGCAGGGCAGTCTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGAGGGTCCGGCCACCAGAAAATTTGCCCAGCTTTGCT   95

TGTTGGCCATGGGTGACCTCTCATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCTGGAGGGGGCT  190
          M  G  D  L  S  S  L  T  P  G  G  S  M  G  L  Q  V  N  R  G  S  Q  S  S  L  E  G  A

GCCACCGCCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTACAGCGTCAGCCACCGCGTGAGGCCCTGGTGGGACATCACATCTTG  285
  A  T  A  P  E  P  H  S  L  G  I  L  H  A  S  Y  S  V  S  H  R  V  R  P  W  W  D  I  T  S  C

GCAGCAGTGGACCAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGA  380
  Q  Q  W  T  R  Q  I  L  K  D  V  S  L  Y  V  E  S  G  Q  I  M  C  I  L  G  S  S  G  S  G

CCACGCTGCTGGACGCCATGTCCGGGAGGCTGGGGCGCGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCGCTGCGCCGGGAG  475
  T  T  L  L  D  A  M  S  G  R  L  G  R  A  G  T  F  L  G  E  V  Y  V  N  G  R  A  L  R  R  E

TTCCAGGACTGCTTCTCCTACGTCCTGCAGAGCGACACCCTGCTGAGCAGCCTCACCGTGCGCGAGACGCTGCACTACACCGCGCTGCTGGC  570
  F  Q  D  C  F  S  Y  V  L  Q  S  D  T  L  L  S  S  L  T  V  R  E  T  L  H  Y  T  A  L  L  A

CCGCCGCGGCAATCCCGGCTCCTTCCAGAAGAAGGTGGAGGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGATTGGCA  665
  R  R  G  N  P  G  S  F  Q  K  K  V  E  A  V  M  A  E  L  S  L  S  H  V  A  D  R  L  I  G

ACAGCTTGGGGGGCATTTCCACGGGTGAGCGGCGCCGGGTCTCCATCGCAGCCCAGCTGCTCCAGGATCCTAAGGTCATGCTGTTTGATGAG  760
  Y  S  L  G  G  I  S  T  G  E  R  R  R  V  S  I  A  A  Q  L  L  Q  D  P  K  V  M  L  F  D  E

ACCACAGGCCTGGACTGCATGACTGCTAATCAGATTGTCGTCCTCCTGGTGGAACTGGCTCGCAGGAACCGAATTGTGGTTCTCACCATTCA  855
  T  T  B  L  D  C  M  T  A  N  Q  I  V  V  L  L  V  E  L  A  R  R  N  R  I  V  V  L  T  I  H
```

FIG. 8A.

```
GCCCCGTTCTGAGCTTTTTCAGCTCTTTGACAAAATTGCCATCCTGAGCTTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGGAAATGCTTG  950
 P  R  S  E  L  F  Q  L  F  D  K  I  A  I  L  S  F  G  E  L  I  F  C  G  T  P  A  E  M  L

TCTTCAATGACTGCGGTTACCCTTGTCCTGAACATTCAAACCCTTTTGACTTCTATATGGACCTGACGTCAGTGGATACCCAAAGCAAGGAA 1045
 F  F  N  D  C  G  Y  P  C  P  E  H  S  N  P  F  D  F  Y  M  D  L  T  S  V  D  T  Q  S  K  E

GAAATAGAAACCTCCAAGAGAGTCCAGATGATAGAATCTGCCTACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAAT 1140
  E  I  E  T  S  K  R  V  Q  M  I  E  S  A  Y  K  K  S  A  I  C  H  K  T  L  K  N  I  E  R  M

ACACCTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAAGATTCTCCTGGAGTTTTCTCTAAACTGGGTGTTCTCCTGAGGAGAGTGACAA 1235
 H  L  K  T  L  P  M  V  P  F  K  T  K  D  S  P  G  V  F  S  K  L  G  V  L  L  R  R  V  T

ACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTTTCTTCGTTCTGCGGGTCCGA 1330
 N  L  V  R  N  K  L  A  V  I  T  R  L  L  Q  N  L  I  M  G  L  F  L  L  F  F  V  L  R  V  R

AATGTGCTAAAGGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCAGTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAA 1425
  N  V  L  K  G  A  I  Q  D  R  V  G  L  L  Y  Q  F  V  Q  A  T  P  Y  T  G  M  L  N  A  V  N

GTTTCCCGTGCTGCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGAAGTGGCAGATGATGCTGGCCTATGCACTGCACGTCC 1520
  F  P  V  L  R  A  V  S  D  Q  E  S  Q  D  G  L  Y  Q  K  W  Q  M  M  L  A  Y  A  L  H  V

CCTTCAGCGTTGTTGCCACCATGATTTTCAGCAGTGTGTGCTACTGGACGCTGGGCTTACATCCTGAGGTTGCCCGATTTGGATATTTTTCT 1615
 P  F  S  V  V  A  T  M  I  F  S  S  V  C  Y  W  T  L  G  L  H  P  E  V  A  R  F  G  Y  F  S

GCTCTCTTGGCCCCCCACTTAATTGGTGAATTTCTAACTCTTGTGCTACTTGGTATCGTCCAAAATCCAAATATAGTCAACAGTGTAGTGGC 1710
  A  L  L  A  P  H  L  I  G  E  F  L  T  L  V  L  L  G  I  V  Q  N  P  N  I  V  N  S  V  V  A

GCTGTCCATTGCGGGGGTGCTTGTTGGATCTGGATTCCTCAGAAACATACAAGAAATGCCCATTCCTTTTAAAATCATCAGTTATTTTACAT 1805
  L  S  I  A  G  V  L  V  G  S  G  F  L  R  N  I  Q  E  M  P  I  P  F  K  I  I  S  Y  F  T

AAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATGTTTCTGTGACAACTAATCCA 1900
 Q  K  Y  C  S  E  I  L  V  V  N  E  F  Y  G  L  N  F  T  C  G  S  S  N  V  S  V  T  T  N  P
```

FIG. 8B.

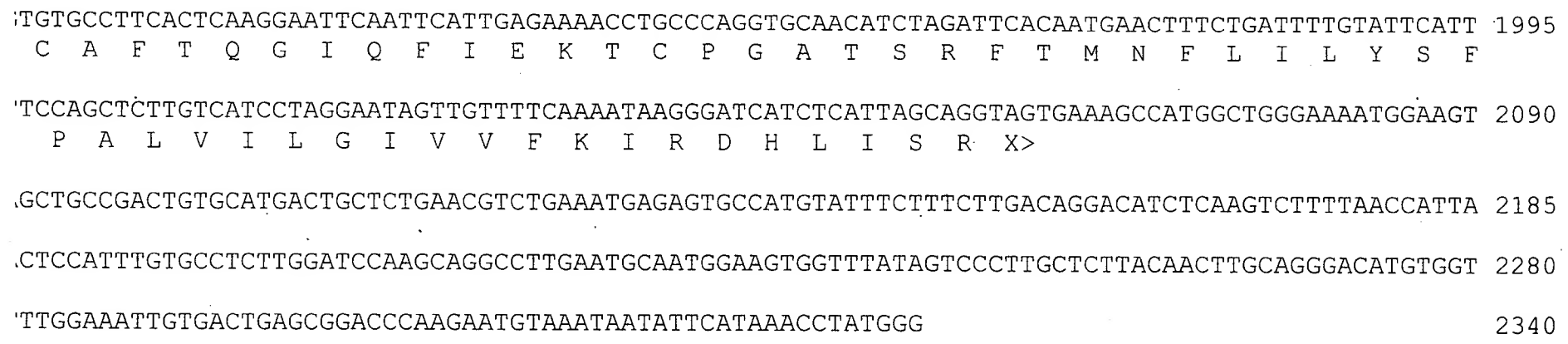


FIG. 8C.

Appln. No.: 09/837,992
Filed: April 18, 2001
SITOSTEROLEMIA SUSCEPTIBILITY GENE (SSG): COMPOSITIONS AND METHODS OF USE
Replacement Sheet

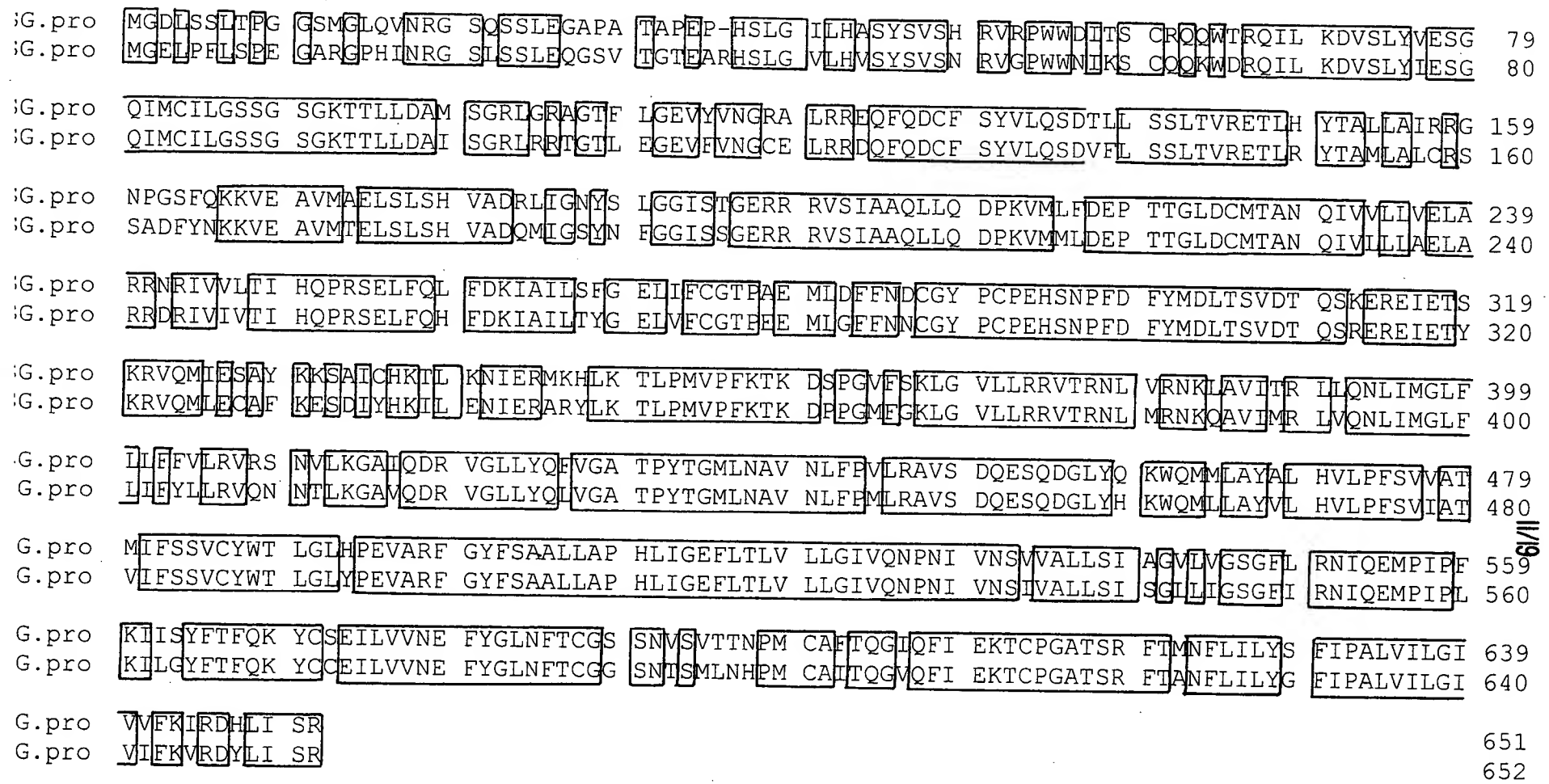


FIG. 9.

Appln. No.: 09/837,992
Filed: April 18, 2001
SITOSTEROLEMIA SUSCEPTIBILITY GENE (SSG): COMPOSITIONS AND METHODS OF USE
Replacement Sheet

```
Reference Number: 6711
Stanford RH Panel: TNG4
Lowest LDD Reported: 5
Chromosome Value: 0

Results for HT

Submitted
Vector:0001000000000100010000101001000000010000001000100
0000000010000000000001000000000001000100

# SHGCNAME CHROM# LOD_SCORE DIST.(cRs)

1 SHGC-36672 2 7.52 35
Vector:00000000R000010101001000100111000001000000100010000
000000101000000000000100000000R01000100

2 SHGC-8189 2 6.53 44
Vector:000000001000010101001000100111000001000000100010000
000000101000000000000100000000101000100

3 SHGC-699 2 6.03 48
Vector:000100000000010001000010100101001000010001100010000
100000101000000000000000010000011000100

The number of markers searched was 32440
```

FIG. 10.

Esophagus
Stomach
Duodenum
Jejunum
Ileum
Cecum
Ascending Colon
Transverse Colon
Descending Colon
Rectum
Small Intestine
Stomach
Rectum
Liver
Jejunum
Ileum
Ileocecum
Esophagus
Duodenum
T. Colon
D. Colon
A. Colon
Cecum

FIG. 11.

Brain
Heart
Kidney
Liver
Lung
Pancreas
Placenta
S. Muscle
Colon
Ovary
PBL
Prostate
S. Intestine
Spleen
Testis
Thymus

FIG. 12.

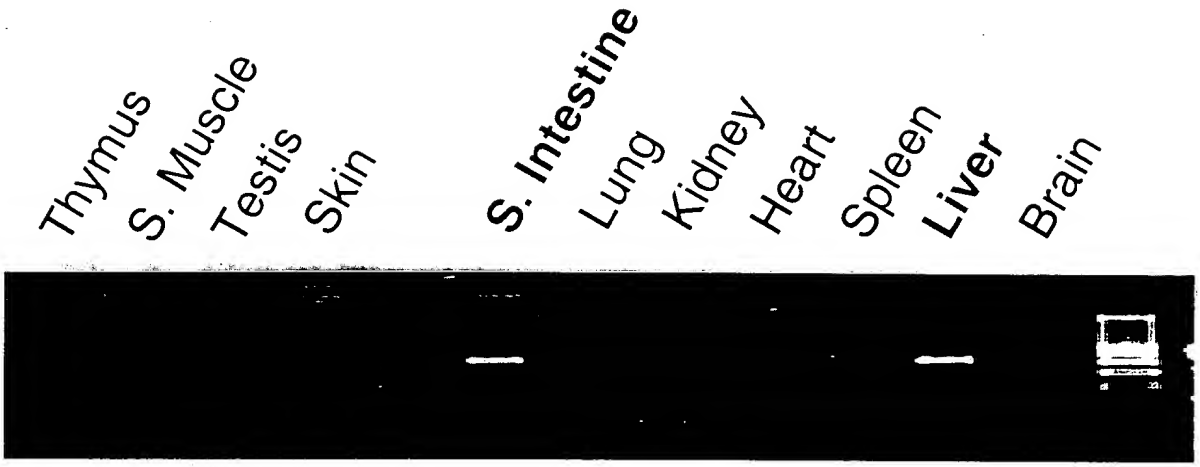

Thymus
S. Muscle
Testis
Skin
S. Intestine
Lung
Kidney
Heart
Spleen
Liver
Brain

FIG. 13.

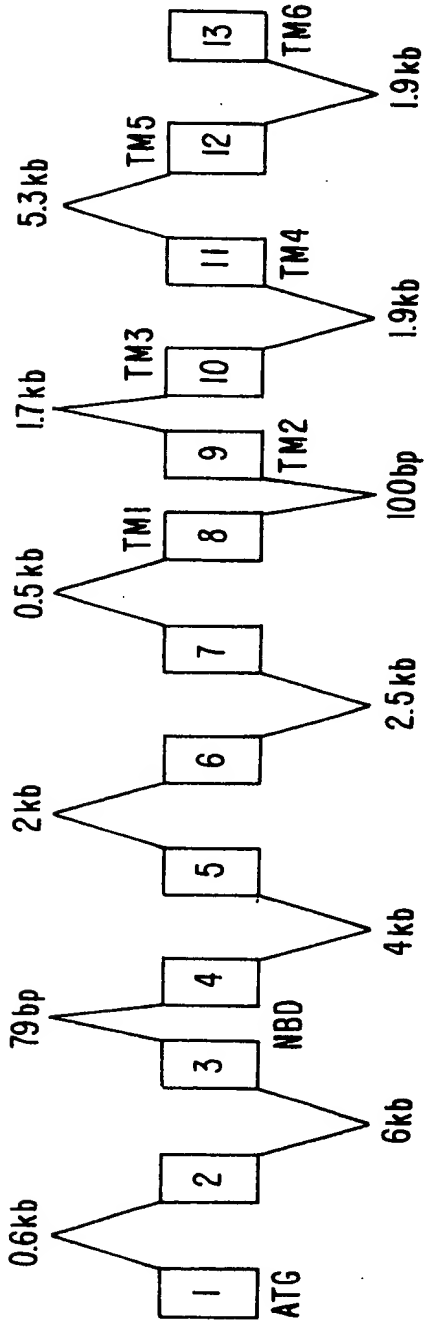

1
2
3
4
5
6
7
8
9
10
11
12
13
ATG
NBD
TM1
TM2
TM3
TM4
TM5
TM6
0.6kb
6kb
79bp
4kb
2kb
2.5kb
0.5kb
100bp
1.7kb
1.9kb
5.3kb
1.9kb

FIG. 14A.

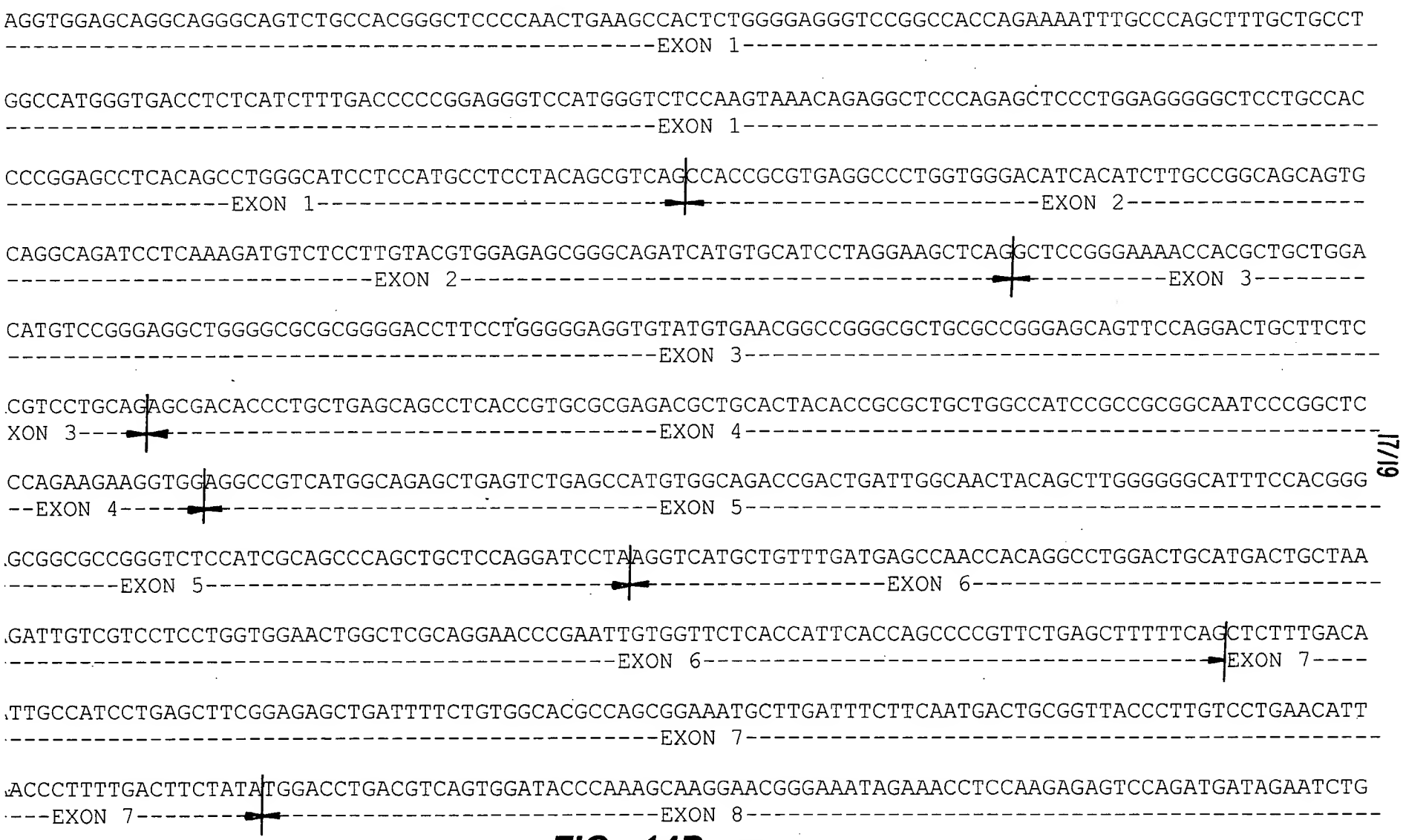
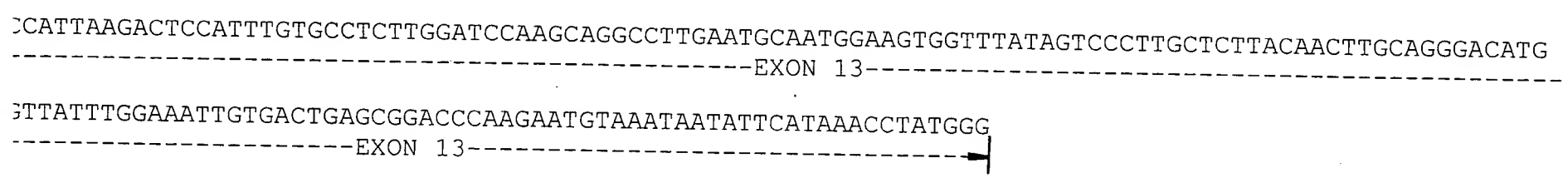

AGGTGGAGCAGGCAGGGCAGTCTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGAGGGTCCGGCCACCAGAAAATTTGCCCAGCTTTGCTGCCT
EXON 1
GGCCATGGGTGACCTCTCATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCTGGAGGGGGCTCCTGCCAC
EXON 1
CCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCTCCTACAGCGTCAGCCACCGCGTGAGGCCCTGGTGGGACATCACATCTTGCCGGCAGCAGTG
EXON 1
EXON 2
CAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAAACCACGCTGCTGGA
EXON 2
EXON 3
CATGTCCGGGAGGCTGGGGCGCGCGGGGACCTTCCTGGGGGAGGTGTATGTGAACGGCCGGGCGCTGCGCCGGGAGCAGTTCCAGGACTGCTTCTC
EXON 3
CGTCCTGCAGAGCGACACCCTGCTGAGCAGCCTCACCGTGCGCGAGACGCTGCACTACACCGCGCTGCTGGCCATCCGCCGCGGCAATCCCGGCTC
XON 3
EXON 4
CCAGAAGAAGGTGGAGGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGATTGGCAACTACAGCTTGGGGGGCATTTCCACGGG
EXON 4
EXON 5
GCGGCGCCGGGTCTCCATCGCAGCCCAGCTGCTCCAGGATCCTAAGGTCATGCTGTTTGATGAGCCAACCACAGGCCTGGACTGCATGACTGCTAA
EXON 5
EXON 6
GATTGTCGTCCTCCTGGTGGAACTGGCTCGCAGGAACCCGAATTGTGGTTCTCACCATTCACCAGCCCCGTTCTGAGCTTTTTCAGCTCTTTGACA
EXON 6
EXON 7
TTGCCATCCTGAGCTTCGGAGAGCTGATTTTCTGTGGCACGCCAGCGGAAATGCTTGATTTCTTCAATGACTGCGGTTACCCTTGTCCTGAACATT
EXON 7
ACCCTTTTGACTTCTATATGGACCTGACGTCAGTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGATAGAATCTG
EXON 7
EXON 8

FIG. 14B. *(1 OF 3)*


ACAAGAAATCAGCAATTTGTCATAAAACTTTGAAGAATATTGAAAGAATGAAACACCTGAAAACGTTACCAATGGTTCCTTTCAAAACCAAAGATT
EXON 8
CTGGAGTTTTCTCTAAACTGGGTGTTCTCCTGAGGAGAGTGACAAGAAACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATC
EXON 8
EXON 9
TCATGGGTTTGTTCCTCCTTTTCTTCGTTCTGCGGGTCCGAAGCAATGTGCTAAAGGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCAGTTTG
EXON 9
GCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAATCTGTTTCCCGTGCTGCGAGCTGTCAGCGACCAGGAGAGTCAGGACGGCCTCTACCAGA
EXON 9
EXON 10
GGCAGATGATGCTGGCCTATGCACTGCACGTCCTCCCCTTCAGCGTTGTTGCCACCATGATTTTCAGCAGTGTGTGCTACTGGACGCTGGGCTTAC
EXON 10
EXON 11
CAAATATAGTCAACAGTGTAGTGGCTCTGCTGTCCATTGCGGGGGTGCTTGTTGGATCTGGATTCCTCAGAAACATACAAGAAATGCCCATTCCTT
EXON 11
EXON 12
AAATCATCAGTTATTTTACATTCCAAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATG
EXON 12
EXON 13
CTGTGACAACTAATCCAATGTGTGCCTTCACTCAAGGAATTCAATTCATTGAGAAAACCTGCCCAGGTGCAACATCTAGATTCACAATGAACTTTC
EXON 13
TTTTGTATTCATTTATTCCAGCTCTTGTCATCCTAGGAATAGTTGTTTTCAAAATAAGGGATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTGG
EXON 13
AATGGAAGTGAAGCTGCCGACTGTGCATGACTGCTCTGAACGTCTGAAATGAGAGTGCCATGTATTTCTTTCTTGACAGGACATCTCAAGTCTTTT
EXON 13

FIG. 14B. *(2 OF 3)*



EXON NUMBER	EXON SIZE	5′ SPLICING SITE	3′ SPLICING SITE	INTRON SIZE
1			GCGTCAGgtaaggcag	-600bp
2	124	cctttaaagCCACCGC	AGCTCAGgtaagcttg	~6kb
3	137	gccccgcagGCTCCGG	CCTGCAGgtgggcgcg	74bp
4	103	ctcctgcagAGCGACA	AAGGTGGgtgcagccc	~4kb
5	129	tgcaggtggAGGCCGT	GATCCTAgtaagtggc	~2kb
6	140	tgctggcagAGGTCAT	TTTTCAGgtaagaggt	~2.5kb
7	130	tctggtcagCTCTTTG	TTCTATAgtaagtttt	~0.5kb
8	214	aacttttagTGGACCT	TCCTGAGgtaagaggc	100bp
9	206	tgttttcagGAGAGTG	AATCTGTgtaagtgcc	~1.7kb
10	139	catccccagTTCCCGT	GCTACTGgtgagggtt	~1.9kb
11	186	cttttctagGACGCTG	TCCTCAGgtaagatat	~5.3kb
12	113	tttcttaagAAACATA	ACTTGTGgtaagtatt	~1.2kb
13		ccttgacagGCAGCTC		
TOTAL				~25.9kb

GENIC SEQUENCES IN CAPITAL LETTER

FIG. 14B. *(3 0F 3)*

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SITOSTEROLEMIA SUSCEPTIBILITY GENE (SSG): COMPOSITIONS AND METHODS OF USE
Replacement Sheet